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NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2		"Ask CAS" for self-help around the clock
NEWS 3	Jun 03	New e-mail delivery for search results now available
NEWS 4	Aug 08	PHARMAMarketLetter(PHARMAML) - new on STN
NEWS 5	Aug 19	Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN
NEWS 6	Aug 26	Sequence searching in REGISTRY enhanced
NEWS 7	Sep 03	JAPIO has been reloaded and enhanced
NEWS 8	Sep 16	Experimental properties added to the REGISTRY file
NEWS 9	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS 10	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS 11	Oct 24	BEILSTEIN adds new search fields
NEWS 12	Oct 24	Nutraceuticals International (NUTRACEUT) now available on STN
NEWS 13	Nov 18	DKILIT has been renamed APOLLIT
NEWS 14	Nov 25	More calculated properties added to REGISTRY
NEWS 15	Dec 04	CSA files on STN
NEWS 16	Dec 17	PCTFULL now covers WP/PCT Applications from 1978 to date
NEWS 17	Dec 17	TOXCENTER enhanced with additional content
NEWS 18	Dec 17	Adis Clinical Trials Insight now available on STN
NEWS 19	Jan 29	Simultaneous left and right truncation added to COMPENDEX, ENERGY, INSPEC
NEWS 20	Feb 13	CANCERLIT is no longer being updated
NEWS 21	Feb 24	METADEX enhancements
NEWS 22	Feb 24	PCTGEN now available on STN
NEWS 23	Feb 24	TEMA now available on STN
NEWS 24	Feb 26	NTIS now allows simultaneous left and right truncation
NEWS 25	Feb 26	PCTFULL now contains images
NEWS 26	Mar 04	SDI PACKAGE for monthly delivery of multifile SDI results
NEWS 27	Mar 20	EVENTLINE will be removed from STN
NEWS 28	Mar 24	PATDPAFULL now available on STN
NEWS 29	Mar 24	Additional information for trade-named substances without structures available in REGISTRY
NEWS 30	Apr 11	Display formats in DGENE enhanced
NEWS 31	Apr 14	MEDLINE Reload
NEWS 32	Apr 17	Polymer searching in REGISTRY enhanced
NEWS 33	Jun 13	Indexing from 1947 to 1956 added to records in CA/CAPLUS
NEWS 34	Apr 21	New current-awareness alert (SDI) frequency in WPIDS/WPINDEX/WPIX
NEWS 35	Apr 28	RDISCLOSURE now available on STN
NEWS 36	May 05	Pharmacokinetic information and systematic chemical names added to PHAR
NEWS 37	May 15	MEDLINE file segment of TOXCENTER reloaded
NEWS 38	May 15	Supporter information for ENCOMPPAT and ENCOMPLIT updated
NEWS 39	May 16	CHEMREACT will be removed from STN
NEWS 40	May 19	Simultaneous left and right truncation added to WSCA
NEWS 41	May 19	RAPRA enhanced with new search field, simultaneous left and right truncation
NEWS 42	Jun 06	Simultaneous left and right truncation added to CBNB

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 NEWS 43  Jun 06  PASCAL enhanced with additional data
 NEWS 44  Jun 20  2003 edition of the FSTA Thesaurus is now available
 NEWS 45  Jun 25  HSDB has been reloaded

 NEWS EXPRESS  April 4 CURRENT WINDOWS VERSION IS V6.01a, CURRENT
               MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
               AND CURRENT DISCOVER FILE IS DATED 01 APRIL 2003
 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS INTER    General Internet Information
 NEWS LOGIN    Welcome Banner and News Items
 NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
 NEWS WWW      CAS World Wide Web Site (general information)

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FILE 'HOME' ENTERED AT 14:38:04 ON 07 JUL 2003

=> file medline, biosis, embase, dgene, jicst, fsta, wpids
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
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FILE 'MEDLINE' ENTERED AT 14:38:52 ON 07 JUL 2003

FILE 'BIOSIS' ENTERED AT 14:38:52 ON 07 JUL 2003
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FILE 'WPIDS' ENTERED AT 14:38:52 ON 07 JUL 2003
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=> s tryptophan fluorescence
L1         5132 TRYPTOPHAN FLUORESCENCE

=> s efp
L2          551 EFP

=> s l2 and l1
L3            0 L2 AND L1

=> s l1 and measurement
L4          166 L1 AND MEASUREMENT

=> s l4 and l2
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L5 0 L4 AND L2

=> s S. aureus EFP
L6 0 S. AUREUS EFP

=> s E. coli EFP
L7 3 E. COLI EFP

=> d l7 ti abs ibib tot

L7 ANSWER 1 OF 3 MEDLINE
TI The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AB The virulence of Agrobacterium tumefaciens depends on both chromosome- and Ti plasmid-encoded gene products. In this study, we characterize a chromosomal locus, chvH, previously identified by TnphoA mutagenesis and shown to be required for tumor formation. Through DNA sequencing and comparison of the sequence with identified sequences in the database, we show that this locus encodes a protein similar in sequence to elongation factor P, a protein thought to be involved in peptide bond synthesis in Escherichia coli. The analysis of vir-lacZ and vir-phoA translational fusions as well as Western immunoblotting revealed that the expression of Vir proteins such as VirE2 was significantly reduced in the chvH mutant compared with the wild-type strain. The **E. coli efp** gene complemented detergent sensitivity, virulence, and expression of VirE2 in the chvH mutant, suggesting that chvH and efp are functionally homologous. As expected, ChvH exerts its activity at the posttranscriptional level. Southern analysis suggests that the gene encoding this elongation factor is present as a single copy in A. tumefaciens. We constructed a chvH deletion mutant in which a 445-bp fragment within its coding sequence was deleted and replaced with an omega fragment. On complex medium, this mutant grew more slowly than the wild-type strain, indicating that elongation factor P is important but not essential for the growth of Agrobacterium.
ACCESSION NUMBER: 2001086878 MEDLINE
DOCUMENT NUMBER: 20566665 PubMed ID: 11114898
TITLE: The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AUTHOR: Peng W T; Banta L M; Charles T C; Nester E W
CORPORATE SOURCE: Department of Microbiology, University of Washington, Seattle, Washington 98195-7242, USA.
CONTRACT NUMBER: GM32618 (NIGMS)
SOURCE: JOURNAL OF BACTERIOLOGY, (2001 Jan) 183 (1) 36-45. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF177860
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010118

L7 ANSWER 2 OF 3 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AB The virulence of Agrobacterium tumefaciens depends on both chromosome- and Ti plasmid-encoded gene products. In this study, we characterize a chromosomal locus, chvH, previously identified by TnphoA mutagenesis and shown to be required for tumor formation. Through DNA sequencing and comparison of the sequence with identified sequences in the database, we show that this locus encodes a protein similar in sequence to elongation factor P, a protein thought to be involved in peptide bond synthesis in

Escherichia coli. The analysis of vir-lacZ and vir-phoA translational fusions as well as Western immunoblotting revealed that the expression of Vir proteins such as VirE2 was significantly reduced in the chvH mutant compared with the wild-type strain. The **E. coli efp** gene complemented detergent sensitivity, virulence, and expression of VirE2 in the chvH mutant, suggesting that chvH and efp are functionally homologous. As expected, ChvH exerts its activity at the posttranscriptional level. Southern analysis suggests that the gene encoding this elongation factor is present as a single copy in A. tumefaciens. We constructed a chvH deletion mutant in which a 445-bp fragment within its coding sequence was deleted and replaced with an omega fragment. On complex medium, this mutant grew more slowly than the wild-type strain, indicating that elongation factor P is important but not essential for the growth of Agrobacterium.

ACCESSION NUMBER: 2001:61207 BIOSIS
DOCUMENT NUMBER: PREV200100061207
TITLE: The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AUTHOR(S): Peng, Wen-Tao; Banta, Lois M.; Charles, Trevor C.; Nester, Eugene W. (1)
CORPORATE SOURCE: (1) Department of Microbiology, University of Washington, Seattle, WA, 98195-7242: gnester@u.washington.edu USA
SOURCE: Journal of Bacteriology, (January, 2001) Vol. 183, No. 1, pp. 36-45. print.
ISSN: 0021-9193.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L7 ANSWER 3 OF 3 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
TI The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AB The virulence of Agrobacterium tumefaciens depends on both chromosome- and Ti plasmid-encoded gene products. In this study, we characterize a chromosomal locus, chvH, previously identified by TnphoA mutagenesis and shown to be required for tumor formation. Through DNA sequencing and comparison of the sequence with identified sequences in the database, we show that this locus encodes a protein similar in sequence to elongation factor P, a protein thought to be involved in peptide bond synthesis in Escherichia coli. The analysis of vir-lacZ and vir-phoA translational fusions as well as Western immunoblotting revealed that the expression of Vir proteins such as VirE2 was significantly reduced in the chvH mutant compared with the wild-type strain. The **E. coli efp** gene complemented detergent sensitivity, virulence, and expression of VirE2 in the chvH mutant, suggesting that chvH and efp are functionally homologous. As expected, ChvH exerts its activity at the posttranscriptional level. Southern analysis suggests that the gene encoding this elongation factor is present as a single copy in A. tumefaciens. We constructed a chvH deletion mutant in which a 445-bp fragment within its coding sequence was deleted and replaced with an omega fragment. On complex medium, this mutant grew more slowly than the wild-type strain, indicating that elongation factor P is important but not essential for the growth of Agrobacterium.

ACCESSION NUMBER: 2001002700 EMBASE
TITLE: The chvH locus of Agrobacterium encodes a homologue of an elongation factor involved in protein synthesis.
AUTHOR: Peng W.-T.; Banta L.M.; Charles T.C.; Nester E.W.
CORPORATE SOURCE: E.W. Nester, Department of Microbiology, Box 357242, University of Washington, Seattle, WA 98195-7242, United States. gnester@u.washington.edu
SOURCE: Journal of Bacteriology, (2001) 183/1 (36-45).
Refs: 55
ISSN: 0021-9193 CODEN: JOBAAY
COUNTRY: United States

DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

=> s E. Coli EFP and tryptophan fluorescence
L8 0 E. COLI EFP AND TRYPTOPHAN FLUORESCENCE

=> s compounds and bind efp
6 FILES SEARCHED...
L9 1 COMPOUNDS AND BIND EFP

=> d l9 ti abs ibib tot

L9 ANSWER 1 OF 1 WPIDS (C) 2003 THOMSON DERWENT
TI Identifying a compound which modulates the activity of prokaryotic elongation factor p (efp) for screening for **compounds** which can be used as antibiotics comprises contacting efp with a compound and determining if efp activity is modified.
AN 2000-524303 [47] WPIDS
AB WO 200045177 A UPAB: 20000925
NOVELTY - A method (M1) for identifying a compound which modulates the activity of efp comprises contacting efp with a compound and determining whether the compound modifies activity of efp.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(1) a method (M2) for identifying a compound which modulates efp activity comprising:
(a) contacting a cell containing efp with a compound identified by M1; and
(b) determining whether the compound inhibits cell growth;
(2) a method (M3) for identifying a compound which modulates efp activity comprising:
(a) contacting a composition comprising efp, N-formylmethionyl-tRNA (fMet-tRNA), 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3 with a compound; and
(b) determining whether the compound allows fMet-tRNA to bind to a complex formed through the interaction of efp, 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3;
(3) a method (M4) for identifying a compound which modulates efp activity comprising:
(a) contacting efp with prokaryotic 30S subunit or 70S ribosome to form a composition;
(b) contacting the composition with a compound; and
(c) determining whether the compound binds to efp in association with the 30S subunit or 70S ribosome or interferes with the binding of efp and the 30S subunit or 70S ribosome;
(4) a method (M5) for identifying a compound which modulates efp activity comprising:
(a) contacting efp with a composition comprising either 50S subunit or 70S ribosome, a tRNA fragment comprising CACCA-radiolabeled amino acid and a peptide bond donor to form a second composition;
(b) contacting the second composition with the compound; and
(c) determining whether the compound inhibits the first peptide bond reaction;
(5) a method (M6) for identifying a compound which modulates efp activity comprising:
(a) contacting a cell or composition containing efp with a detectably labelled oxazolidinone compound known to **bind efp**;
(b) contacting the composition or cell with an unlabelled compound; and
(c) determining whether the unlabelled compound displaces the labelled oxazolidinone compound from the complex;

(6) a method (M7) for identifying a compound which modulates efp but not eukaryotic eIF5A activity comprising:

(a) determining whether the compound modulates the activity of prokaryotic efp by M1 - M7;

(b) contacting eIF5A with a composition comprising methionyl-tRNA (Met-tRNA), 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C, eIF-4D and a peptide bond donor to form a second composition;

(c) contacting the second composition with a compound; and

(d) determining whether the compound inhibits the first peptide bond reaction of a complex formed through the interaction of eIF5A, Met-tRNA, 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C and eIF-4D; and

(7) modulating the activity of prokaryotic efp, the 30S subunit, 50S subunit, 70S ribosome or L16 protein comprising contacting the efp or cell or cell preparation containing the efp, the 30S subunit, 50S subunit, 70S ribosome or L16 protein with an oxazolidinone compound.

USE - To screen for **compounds** which modulate ribosome mediated peptide bond formation. These screening assays can be used to discover new and useful antibiotics.

ADVANTAGE - This screening method is more rapid and direct than currently available methods.

Dwg.0/0

ACCESSION NUMBER: 2000-524303 [47] WPIDS
DOC. NO. NON-CPI: N2000-387540
DOC. NO. CPI: C2000-155724
TITLE: Identifying a compound which modulates the activity of prokaryotic elongation factor p (efp) for screening for **compounds** which can be used as antibiotics comprises contacting efp with a compound and determining if efp activity is modified.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): MAROTTI, K R; POORMAN, R A; SHINABARGER, D L; WELLS, P A
PATENT ASSIGNEE(S): (PHAA) PHARMACIA & UPJOHN; (PHAA) PHARMACIA & UPJOHN CO
COUNTRY COUNT: 87
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000045177	A1	20000803	(200047)*	EN	52
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW					
AU 9942246	A	20000818	(200057)		
EP 1147422	A1	20011024	(200171)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
JP 2002535680	W	20021022	(200301)		63
US 6511813	B1	20030128	(200311)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000045177	A1	WO 1999-US12073	19990528
AU 9942246	A	AU 1999-42246	19990528
EP 1147422	A1	EP 1999-926086	19990528
		WO 1999-US12073	19990528
JP 2002535680	W	WO 1999-US12073	19990528
		JP 2000-596378	19990528
US 6511813	B1 Provisional	US 1999-117473P	19990127

Div ex	US 1999-322732	19990528
	US 2000-704321	20001102

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9942246	A	Based on	WO 200045177
EP 1147422	A1	Based on	WO 200045177
JP 2002535680	W	Based on	WO 200045177

PRIORITY APPLN. INFO: US 1999-117473P 19990127; US 1999-322732 19990528; US 2000-704321 20001102

=> d his

(FILE 'HOME' ENTERED AT 14:38:04 ON 07 JUL 2003)

FILE 'MEDLINE, BIOSIS, EMBASE, DGENE, JICST-EPLUS, FSTA, WPIDS' ENTERED AT 14:38:52 ON 07 JUL 2003

L1 5132 S TRYPTOPHAN FLUORESCENCE
L2 551 S EFP
L3 0 S L2 AND L1
L4 166 S L1 AND MEASUREMENT
L5 0 S L4 AND L2
L6 0 S S. AUREUS EFP
L7 3 S E. COLI EFP
L8 0 S E. COLI EFP AND TRYPTOPHAN FLUORESCENCE
L9 1 S COMPOUNDS AND BIND EFP

=> s fluorescence and increase activity
4 FILES SEARCHED...
L10 5 FLUORESCENCE AND INCREASE ACTIVITY

=> d l10 ti abs ibib tot

L10 ANSWER 1 OF 5 MEDLINE
TI Activity of copper-substituted carboxypeptidase A toward oligopeptides and depsipeptides.
AB Cu(II)-substituted carboxypeptidase A catalyzes the hydrolysis of oligopeptides and their depsipeptide (ester) analogues. Stopped-flow **fluorescence** assays demonstrate that relative to the zinc enzyme the Cu enzyme can have kcat/Km values up to 24% toward esters but only up to 2.5% toward the corresponding peptides. Adding Zn(II) to the copper enzyme reveals a slow exchange process that correlates with an increase in peptidase activity and with changes in the Cu(II) electron paramagnetic resonance spectra. Low concentrations of 1,10-phenanthroline (OP) (0.1-2.5 microM) markedly **increase activity** toward furanacryloyl-Phe-Phe (up to 8% of the zinc enzyme), but higher concentrations inhibit, resulting in complete inhibition at 0.8 mM OP. The non-metal-binding, hydrophobic analogues m- and p-phenanthroline are only activators of peptide hydrolysis, even at 1 mM. Activation is likely due to a modifier binding to a hydrophobic locus and either displacing an inhibitory peptide binding mode or inducing a conformational change in the active site.
ACCESSION NUMBER: 86243369 MEDLINE
DOCUMENT NUMBER: 86243369 PubMed ID: 3013305
TITLE: Activity of copper-substituted carboxypeptidase A toward oligopeptides and depsipeptides.
AUTHOR: Schaffer A; Auld D S
CONTRACT NUMBER: GM-24967 (NIGMS)
SOURCE: BIOCHEMISTRY, (1986 May 6) 25 (9) 2476-9.
Journal code: 0370623. ISSN: 0006-2960.

PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198608
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 20000303
Entered Medline: 19860801

L10 ANSWER 2 OF 5 MEDLINE
TI Rat mammary carcinoma cells secrete active collagenase and activate latent enzyme in the stroma via plasminogen activator.
AB A spontaneous mammary adenocarcinoma (AC) from an inbred female rat was investigated with regard to secretion of neutral proteases. Cultures of neoplastic epithelial cells derived from the tumour secreted an enzyme that fulfilled the criteria for a specific collagenase. In contrast to cultures of non-neoplastic cells, tumour collagenase was present as an active enzyme, since treatment with trypsin or p-aminophenylmercuric acetate (APMA) did not **increase activity**. The neoplastic cells were also prolific producers of plasminogen activator (PA). Dexamethasone (Dex) (10(-6)M) markedly reduced the levels of both enzymes. Addition of tranexamic acid (TA), an inhibitor of plasmin and of plasminogen activation, did not affect collagenase activity, even at 10(-1)M TA, nor did latent collagenase accumulate. Latent collagenase was secreted in culture by normal fibroblasts from neonatal rat lungs. This latent enzyme was activated by the addition of tumour cell medium plus plasminogen, but this effect was inhibited by the addition of TA. These results demonstrate that the neoplastic cells themselves secrete collagenase as an active enzyme. PA is also secreted, is not involved with tumour collagenase, but is capable, in the presence of plasminogen, of activating latent collagenase produced by the non-neoplastic cells within the tumour or in the surrounding tissue. This tumour possesses potent collagenolytic ability in vitro which may be partly responsible for its rapid invasion in vivo.
ACCESSION NUMBER: 82074923 MEDLINE
DOCUMENT NUMBER: 82074923 PubMed ID: 6273336
TITLE: Rat mammary carcinoma cells secrete active collagenase and activate latent enzyme in the stroma via plasminogen activator.
AUTHOR: O'Grady R L; Upfold L I; Stephens R W
SOURCE: INTERNATIONAL JOURNAL OF CANCER, (1981 Oct 15) 28 (4) 509-15.
Journal code: 0042124. ISSN: 0020-7136.
PUB. COUNTRY: Denmark
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198202
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19970203
Entered Medline: 19820222

L10 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Protection against photooxidative damage provided by enzymatic and non-enzymatic antioxidant system in sorghum seedlings.
AB Effect of photoinhibition of sorghum leaves and isolated chloroplasts on chlorophyll **fluorescence**, peroxidation of thylakoid lipids and activity of antioxidant enzymes were studied. Photoinhibition of intact leaves and isolated chloroplasts decreased Fv/Fm ratio and qP, while qN increased. Photoinhibitory damage was more at 5degreeC than at 30degree or 50degreeC. Peroxidation of thylakoid lipids was 5 times greater when photoinhibited at 50degreeC compared to control. Photoinhibition of chloroplasts under low oxygen condition or when supplemented with anti-oxidants (beta-carotene, ascorbate and GSH) resulted in significantly

less damage to photosynthesis (Fv/Fm ratio) and peroxidation level. Photoinhibition also resulted in many fold increase in the activity of superoxide dismutase (SOD) and ascorbate peroxidase (APX) and decrease in catalase. Data presented here suggest that photoinhibition resulted in production of oxygen radicals and photoinhibition of chloroplasts in the presence of low oxygen level or when supplemented with antioxidants decreased the damage to Fv/Fm ratio and peroxidation level to a great extent since former prevented the formation of oxygen radicals and later could scavenge the oxygen radicals thus the protection. **Increase activity** of SOD and APX may also be to metabolise the oxygen radicals produced during photoinhibition treatment, thereby, protecting the seedlings against photooxidative damage.

ACCESSION NUMBER: 2003:23965 BIOSIS
DOCUMENT NUMBER: PREV200300023965
TITLE: Protection against photooxidative damage provided by enzymatic and non-enzymatic antioxidant system in sorghum seedlings.
AUTHOR(S): Sankhalkar, Sangeeta; Sharma, Prabhat Kumar (1)
CORPORATE SOURCE: (1) Department of Botany, Goa University, Goa, 403 206, India: pksharma@unigoa.ernet.in India
SOURCE: Indian Journal of Experimental Biology, (November 2002, 2002) Vol. 40, No. 11, pp. 1260-1268. print. ISSN: 0019-5189.
DOCUMENT TYPE: Article
LANGUAGE: English

L10 ANSWER 4 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI ACTIVITY OF COPPER-SUBSTITUTED CARBOXYPEPTIDASE A TOWARD OLIGOPEPTIDES AND DEPSIPEPTIDES.
AB Cu(II)-substituted carboxypeptidase A catalyzes the hydrolysis of oligopeptides and their dipsipeptide (ester) analogues. Stopped-flow **fluorescence** assays demonstrate that relative to the zinc enzyme the Cu enzyme can have kcat/Km values up to 24% toward esters but only up to 2.5% toward the corresponding peptides. Adding Zn(II) to the copper enzyme reveals a slow exchange process that correlates with an increase in peptidase activity and with changes in the Cu(II) electron paramagnetic resonance spectra. Low concentrations of 1,10-phenanthroline (OP) (0.1-2.5 .mu.M) markedly **increase activity** toward furanacryloyl-Phe-Phe (up to 8% of the zinc enzyme), but higher concentrations inhibit, resulting in complete inhibition of 0.8 mM OP. The non-metal binding, hydrophobic analogues m- and p-phenanthroline are only activators of peptide hydrolysis, even at 1 mM. Activation is likely due to a modifier binding to a hydrophobic locus and either displacing an inhibitory peptide binding mode or inducing a conformational change in the active site.

ACCESSION NUMBER: 1986:299477 BIOSIS
DOCUMENT NUMBER: BA82:33383
TITLE: ACTIVITY OF COPPER-SUBSTITUTED CARBOXYPEPTIDASE A TOWARD OLIGOPEPTIDES AND DEPSIPEPTIDES.
AUTHOR(S): SCHAFFER A; AULD D S
CORPORATE SOURCE: DEP. PATHOL., HARVARD MED. SCH., BOSTON, MASS. 02115.
SOURCE: BIOCHEMISTRY, (1986) 25 (9), 2476-2479. CODEN: BICHAW. ISSN: 0006-2960.
FILE SEGMENT: BA; OLD
LANGUAGE: English

L10 ANSWER 5 OF 5 WPIDS (C) 2003 THOMSON DERWENT
TI Assay reagent for determn. of intracellular enzymatic activity in whole cells - contains enzyme-cleavable cpd. that can cross cell membranes and is converted to fluorescent form when cleaved, used for diagnosis, cell classification, disease monitoring, etc..
AN 1997-012099 [01] WPIDS
CR 1998-286965 [25]; 1999-190176 [16]
AB WO 9636729 A UPAB: 19991221

Assay reagent (A) for determining enzymatic activity of a metabolically active whole cell comprises at least one water soluble cpd. (I), or its salt, able to pass through a cell membrane and having (i) a leaving gp. (LG) cleavable by the enzyme and (b) a fluorogenic indicator (II) that is non-fluorescent when bound to LG but is excitable at above 450 nm when LG has been removed. (A) has lower **fluorescence** that the natural **fluorescence** of the cell.

LG is an amino acid, peptide, saccharide, sulphate, phosphate (ester), ester, (poly)nucleotide, nucleic acid, pyrimidine, purine, nucleoside and/or lipid, and after its removal (I) is excitable at pref. 500-600 nm. Esp. where LG is a peptide the concn. of amino acid and peptide impurities in (A) is below 10 ppm, with (A) having background **fluorescence** below 0.1 million photons and ionic strength 0.1-0.3 mu . Specified (II) are rhodamine 110, rhodol, fluorescein or derivs. with 4' or 5'' positions protected. (A) has a background colour below 1000 milliabsorbance units and may also include a buffer (to **increase activity** of target enzyme relative to other enzymes), an activator of target enzyme, inhibitor of other enzymes, solubiliser and/or agent that inhibits a cell pump for expressing extracellular material. Suitable salts of (I) are with acids, e.g. HCl, HNO3, acetic, citric etc.

USE - Analysis of intracellular enzyme activity can be used for genetic studies to detect cell abnormalities, partic. for diagnosis of leukaemia (test cells are lymphocytes or granulocytes) but also cancers in general (including assessment of metastatic potential) microbial infections (partic. AIDS, cytomegalovirus, herpes hepatitis, syphilis and tuberculosis), sepsis, inflammation, immune diseases (including differential diagnosis) and anaemia. The method is also useful for cell classification, esp. differentiating between nucleated and non-nucleated red blood cells; to monitor progress of disease or treatment; to detect cell differentiation and to detect HIV contamination of blood supplies.

ADVANTAGE - (A) are stable for at least 30 days (pref. 1 year) at 4 deg. C, with increase in background **fluorescence** no more than 10%. Compare with known assays for intracellular enzymes, the new method is quicker and can monitor events as they occur (e.g. to provide early indication of tuberculosis infection in AIDS patients).

Dwg.10/18

ABEQ US 5698411 A UPAB: 19980202

Assay reagent (A) for determining enzymatic activity of a metabolically active whole cell comprises at least one water soluble cpd. (I), or its salt, able to pass through a cell membrane and having (i) a leaving gp. (LG) cleavable by the enzyme and (b) a fluorogenic indicator (II) that is non-fluorescent when bound to LG but is excitable at above 450 nm when LG has been removed. (A) has lower **fluorescence** that the natural **fluorescence** of the cell.

LG is an amino acid, peptide, saccharide, sulphate, phosphate (ester), ester, (poly)nucleotide, nucleic acid, pyrimidine, purine, nucleoside and/or lipid, and after its removal (I) is excitable at pref. 500-600 nm. Esp. where LG is a peptide the concn. of amino acid and peptide impurities in (A) is below 10 ppm, with (A) having background **fluorescence** below 0.1 million photons and ionic strength 0.1-0.3 mu . Specified (II) are rhodamine 110, rhodol, fluorescein or derivs. with 4' or 5'' positions protected. (A) has a background colour below 1000 milliabsorbance units and may also include a buffer (to **increase activity** of target enzyme relative to other enzymes), an activator of target enzyme, inhibitor of other enzymes, solubiliser and/or agent that inhibits a cell pump for expressing extracellular material. Suitable salts of (I) are with acids, e.g. HCl, HNO3, acetic, citric etc.

USE - Analysis of intracellular enzyme activity can be used for genetic studies to detect cell abnormalities, partic. for diagnosis of leukaemia (test cells are lymphocytes or granulocytes) but also cancers in general (including assessment of metastatic potential) microbial infections (partic. AIDS, cytomegalovirus, herpes hepatitis, syphilis and tuberculosis), sepsis, inflammation, immune diseases (including differential diagnosis) and anaemia. The method is also useful for cell

classification, esp. differentiating between nucleated and non-nucleated red blood cells; to monitor progress of disease or treatment; to detect cell differentiation and to detect HIV contamination of blood supplies.

ADVANTAGE - (A) are stable for at least 30 days (pref. 1 year) at 4 deg. C, with increase in background **fluorescence** no more than 10%. Compare with known assays for intracellular enzymes, the new method is quicker and can monitor events as they occur (e.g. to provide early indication of tuberculosis infection in AIDS patients).

Dwg.0/0

ACCESSION NUMBER: 1997-012099 [01] WPIDS
CROSS REFERENCE: 1998-286965 [25]; 1999-190176 [16]
DOC. NO. NON-CPI: N1997-010468
DOC. NO. CPI: C1997-003410
TITLE: Assay reagent for determn. of intracellular enzymatic activity in whole cells - contains enzyme-cleavable cpd. that can cross cell membranes and is converted to fluorescent form when cleaved, used for diagnosis, cell classification, disease monitoring, etc..
DERWENT CLASS: B04 D16 S03
INVENTOR(S): BOTT, S E; CARTER, J H; JAFFE, G E; LUCAS, F J; BOTT, S
PATENT ASSIGNEE(S): (COUS) COULTER INT CORP; (COUS) COULTER CORP
COUNTRY COUNT: 21
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9636729	A1	19961121	(199701)*	EN	238
RW: AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA JP					
US 5698411	A	19971216	(199805)		68
EP 832279	A1	19980401	(199817)	EN	
R: CH DE FR GB LI NL					
US 5733719	A	19980331	(199820)		88
US 5776720	A	19980707	(199834)		
US 5849513	A	19981215	(199906)		
US 5871946	A	19990216	(199914)		
JP 11505702	W	19990525	(199931)		222

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9636729	A1		WO 1996-US6860	19960514
US 5698411	A		US 1995-444051	19950518
EP 832279	A1		EP 1996-915790	19960514
			WO 1996-US6860	19960514
US 5733719	A		US 1995-445217	19950518
US 5776720	A		US 1995-443776	19950518
US 5849513	A	Div ex	US 1995-443776	19950518
			US 1997-904400	19970731
US 5871946	A		US 1995-444056	19950518
JP 11505702	W		JP 1996-534975	19960514
			WO 1996-US6860	19960514

FILING DETAILS:

PATENT NO	KIND		PATENT NO
EP 832279	A1	Based on	WO 9636729
JP 11505702	W	Based on	WO 9636729

PRIORITY APPLN. INFO: US 1995-445217 19950518; US 1995-443776 19950518; US 1995-444051 19950518; US 1995-444056 19950518; US 1997-904400 19970731

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=> d his

     (FILE 'HOME' ENTERED AT 14:38:04 ON 07 JUL 2003)

     FILE 'MEDLINE, BIOSIS, EMBASE, DGENE, JICST-EPLUS, FSTA, WPIDS' ENTERED
     AT 14:38:52 ON 07 JUL 2003
L1          5132 S TRYPTOPHAN FLUORESCENCE
L2           551 S EFP
L3             0 S L2 AND L1
L4           166 S L1 AND MEASUREMENT
L5             0 S L4 AND L2
L6             0 S S. AUREUS EFP
L7             3 S E. COLI EFP
L8             0 S E. COLI EFP AND TRYPTOPHAN FLUORESCENCE
L9             1 S COMPOUNDS AND BIND EFP
L10            5 S FLUORESCENCE AND INCREASE ACTIVITY

=> s efp and binding
L11           46 EFP AND BINDING

=> s l11 and fluorescence
L12            5 L11 AND FLUORESCENCE

=> d l12 ti abs ibib tot

L12  ANSWER 1 OF 5     MEDLINE
TI   Transcriptional repression by RING finger protein TIF1 beta that interacts
     with the KRAB repressor domain of KOX1.
AB   Many of the vertebrate zinc finger factors of the Kruppel type (C2H2 zinc
     fingers) contain in their N-terminus a conserved sequence referred to as
     the KRAB (Kruppel-associated box) domain that, when tethered to DNA,
     efficiently represses transcription. Using the yeast two-hybrid system,
     we have isolated an 835 amino acid RING finger (C3HC4 zinc finger)
     protein, TIF1 beta (also named KAP-1), that specifically interacts with
     the KRAB domain of the human zinc finger factor KOX1/ZNF10. TIF1 beta,
     TIF1 alpha, PML and efp belong to a characteristic subgroup of
     RING finger proteins that contain one or two other Cys/His-rich clusters
     (B boxes) and a putative coiled-coil in addition to the classical C3HC4
     RING finger motif (RBCC configuration). Like TIF1 alpha, TIF1 beta also
     contains an additional Cys/His cluster (PHD finger) and a bromo-related
     domain. When tethered to DNA, TIF1 beta can repress transcription in
     transiently transfected mammalian cells both from promoter-proximal and
     remote (enhancer) positions, similarly to the KRAB domain itself. We
     propose that TIF1 beta is a mediator of the transcriptional repression
     exerted by the KRAB domain.
ACCESSION NUMBER:    97169206     MEDLINE
DOCUMENT NUMBER:     97169206   PubMed ID: 9016654
TITLE:               Transcriptional repression by RING finger protein TIF1 beta
                     that interacts with the KRAB repressor domain of KOX1.
AUTHOR:              Moosmann P; Georgiev O; Le Douarin B; Bourquin J P;
                     Schaffner W
CORPORATE SOURCE:    Institut fur Molekularbiologie der Universitat, Abteilung
                     II, Zurich, Switzerland.
SOURCE:              NUCLEIC ACIDS RESEARCH, (1996 Dec 15) 24 (24) 4859-67.
                     Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY:        ENGLAND: United Kingdom
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
OTHER SOURCE:        GENBANK-X97548
ENTRY MONTH:         199703
ENTRY DATE:          Entered STN: 19970321
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Last Updated on STN: 19970321
Entered Medline: 19970311

L12 ANSWER 2 OF 5 MEDLINE
TI Chromosome mapping of human (ZNF147) and mouse genes for estrogen-responsive finger protein (**efp**), a member of the RING finger family.
AB We have previously identified an estrogen-responsive gene, **efp** (estrogen-responsive finger protein), that encodes a putative zinc finger protein (Proc. Natl. Acad. Sci. USA 90: 11117-11121, 1993). The **efp** protein has a RING finger, a variant type of zinc finger motif, B1 box, and B2 box, each having a pair of zinc fingers, present in a family of apparent DNA-**binding** proteins. Some members of this family have transformation capabilities when found in chromosomal translocations. Chromosome mapping of the **efp** gene by **fluorescence** in situ hybridization reveals that human **EFP** (ZNF147) is located at 17q23.1 and that mouse **Efp** is located at 11C. These results provide additional evidence that the mouse 11C region displays conserved synteny with the 17q23.1 region of the human genome.
ACCESSION NUMBER: 95309931 MEDLINE
DOCUMENT NUMBER: 95309931 PubMed ID: 7789997
TITLE: Chromosome mapping of human (ZNF147) and mouse genes for estrogen-responsive finger protein (**efp**), a member of the RING finger family.
AUTHOR: Inoue S; Orimo A; Matsuda Y; Inazawa J; Emi M; Nakamura Y; Hori T; Muramatsu M
CORPORATE SOURCE: Department of Biochemistry, Saitama Medical School, Japan.
SOURCE: GENOMICS, (1995 Jan 20) 25 (2) 581-3.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199507
ENTRY DATE: Entered STN: 19950807
Last Updated on STN: 19950807
Entered Medline: 19950721

L12 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Chromosome mapping of human (ZNF147) and mouse genes for estrogen-responsive finger protein (**efp**), a member of the RING finger family.
AB We have previously identified an estrogen-responsive gene, **efp** (estrogen-responsive finger protein), that encodes a putative zinc finger protein (Proc. Natl. Acad. Sci. USA 90:11117-11121,1993). The **efp** protein has a RING finger, a variant type of zinc finger motif, B1 box, and B2 box, each having a pair of zinc fingers, present in a family of apparent DNA-**binding** proteins. Some members of this family have transformation capabilities when found in chromosomal translocations. Chromosome mapping of the **efp** gene by **fluorescence** in situ hybridization reveals that human **EFP** (ZNF147) is located at 17q23.1 and that mouse **Efp** is located at 11C. These results provide additional evidence that the mouse 11C region displays conserved synteny with the 17q23.1 region of the human genome.
ACCESSION NUMBER: 1995:171884 BIOSIS
DOCUMENT NUMBER: PREV199598186184
TITLE: Chromosome mapping of human (ZNF147) and mouse genes for estrogen-responsive finger protein (**efp**), a member of the RING finger family.
AUTHOR(S): Inoue, Satoshi; Orimo, Akira; Matsuda, Youichi; Inazawa, Johji; Emi, Mitsuru; Nakamura, Yusuke; Hori, Tada-Aki; Muramatsu, Masami (1)
CORPORATE SOURCE: (1) Dep. Biochemistry, Saitama Med. Sch., 38 Moro-Hongo, Moroyama-machi, Iruma-gun, Saitama 350-04 Japan

SOURCE: Genomics, (1995) Vol. 25, No. 2, pp. 581-583.
ISSN: 0888-7543.
DOCUMENT TYPE: Article
LANGUAGE: English

L12 ANSWER 4 OF 5 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
TI Chromosome mapping of human (ZNF147) and mouse genes for estrogen-responsive finger protein (**efp**), a member of the RING finger family.
AB We have previously identified an estrogen-responsive gene, **efp** (estrogen- responsive finger protein), that encodes a putative zinc finger protein (Proc. Natl. Acad. Sci. USA 90: 11117-11121, 1993). The **efp** protein has a RING finger, a variant type of zinc finger motif, B1 box, and B2 box, each having a pair of zinc fingers, present in a family of apparent DNA-**binding** proteins. Some members of this family have transformation capabilities when found in chromosomal translocations. Chromosome mapping of the **efp** gene by **fluorescence** in situ hybridization reveals that human **EFP** (ZNF147) is located at 17q23.1 and that mouse **Efp** is located at 11C. These results provide additional evidence that the mouse 11C region displays conserved synteny with the 17q23.1 region of the human genome.
ACCESSION NUMBER: 95071796 EMBASE
DOCUMENT NUMBER: 1995071796
TITLE: Chromosome mapping of human (ZNF147) and mouse genes for estrogen- responsive finger protein (**efp**), a member of the RING finger family.
AUTHOR: Inoue S.; Orimo A.; Matsuda Y.; Inazawa J.; Emi M.; Nakamura Y.; Hori - T.A.; Muramatsu M.
CORPORATE SOURCE: Department of Biochemistry, Saitama Medical School, 38 Moro-Hongo, Moroyama-machi,Iruma-gun, Saitama 350-04, Japan
SOURCE: Genomics, (1995) 25/2 (581-583).
ISSN: 0888-7543 CODEN: GNMCEP
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English

L12 ANSWER 5 OF 5 WPIDS (C) 2003 THOMSON DERWENT
TI Identifying a compound which modulates the activity of prokaryotic elongation factor p (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified.
AN 2000-524303 [47] WPIDS
AB WO 200045177 A UPAB: 20000925
NOVELTY - A method (M1) for identifying a compound which modulates the activity of **efp** comprises contacting **efp** with a compound and determining whether the compound modifies activity of **efp**.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a method (M2) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a cell containing **efp** with a compound identified by M1; and

(b) determining whether the compound inhibits cell growth;

(2) a method (M3) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a composition comprising **efp**, N-formylmethionyl-tRNA (fMet-tRNA), 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3 with a compound; and

(b) determining whether the compound allows fMet-tRNA to bind to a complex formed through the interaction of **efp**, 30S subunit, 50S, an mRNA containing an AUG sequence and initiation factors 1,2 and 3;

(3) a method (M4) for identifying a compound which modulates **efp** activity comprising:

(a) contacting **efp** with prokaryotic 30S subunit or 70S ribosome to form a composition;

(b) contacting the composition with a compound; and

(c) determining whether the compound binds to **efp** in association with the 30S subunit or 70S ribosome or interferes with the **binding** of **efp** and the 30S subunit or 70S ribosome;

(4) a method (M5) for identifying a compound which modulates **efp** activity comprising:

(a) contacting **efp** with a composition comprising either 50S subunit or 70S ribosome, a tRNA fragment comprising CACCA-radiolabeled amino acid and a peptide bond donor to form a second composition;

(b) contacting the second composition with the compound; and

(c) determining whether the compound inhibits the first peptide bond reaction;

(5) a method (M6) for identifying a compound which modulates **efp** activity comprising:

(a) contacting a cell or composition containing **efp** with a detectably labelled oxazolidinone compound known to bind **efp**;

(b) contacting the composition or cell with an unlabelled compound; and

(c) determining whether the unlabelled compound displaces the labelled oxazolidinone compound from the complex;

(6) a method (M7) for identifying a compound which modulates **efp** but not eukaryotic eIF5A activity comprising:

(a) determining whether the compound modulates the activity of prokaryotic **efp** by M1 - M7;

(b) contacting eIF5A with a composition comprising methionyl-tRNA (Met-tRNA), 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C, eIF-4D and a peptide bond donor to form a second composition;

(c) contacting the second composition with a compound; and

(d) determining whether the compound inhibits the first peptide bond reaction of a complex formed through the interaction of eIF5A, Met-tRNA, 80S ribosome, an mRNA containing an AUG sequence, initiation factors eIF-2, eIF-3, eIF-5, eIF-4C and eIF-4D; and

(7) modulating the activity of prokaryotic **efp**, the 30S subunit, 50S subunit, 70S ribosome or L16 protein comprising contacting the **efp** or cell or cell preparation containing the **efp** , the 30S subunit, 50S subunit, 70S ribosome or L16 protein with an oxazolidinone compound.

USE - To screen for compounds which modulate ribosome mediated peptide bond formation. These screening assays can be used to discover new and useful antibiotics.

ADVANTAGE - This screening method is more rapid and direct than currently available methods.

Dwg.0/0

ACCESSION NUMBER: 2000-524303 [47] WPIDS
DOC. NO. NON-CPI: N2000-387540
DOC. NO. CPI: C2000-155724
TITLE: Identifying a compound which modulates the activity of prokaryotic elongation factor p (**efp**) for screening for compounds which can be used as antibiotics comprises contacting **efp** with a compound and determining if **efp** activity is modified.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): MAROTTI, K R; POORMAN, R A; SHINABARGER, D L; WELLS, P A
PATENT ASSIGNEE(S): (PHAA) PHARMACIA & UPJOHN; (PHAA) PHARMACIA & UPJOHN CO
COUNTRY COUNT: 87
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

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WO 2000045177 A1 20000803 (200047)* EN   52
   RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL
       OA PT SD SE SL SZ UG ZW
    W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB
       GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU
       LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR
       TT UA UG US UZ VN YU ZA ZW
AU 9942246    A  20000818 (200057)
EP 1147422    A1 20011024 (200171)  EN
    R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
       RO SE SI
JP 2002535680 W  20021022 (200301)       63
US 6511813    B1 20030128 (200311)
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APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2000045177	A1		WO 1999-US12073	19990528
AU 9942246	A		AU 1999-42246	19990528
EP 1147422	A1		EP 1999-926086	19990528
			WO 1999-US12073	19990528
JP 2002535680	W		WO 1999-US12073	19990528
			JP 2000-596378	19990528
US 6511813	B1	Provisional	US 1999-117473P	19990127
		Div ex	US 1999-322732	19990528
			US 2000-704321	20001102

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9942246	A	Based on	WO 200045177
EP 1147422	A1	Based on	WO 200045177
JP 2002535680	W	Based on	WO 200045177

PRIORITY APPLN. INFO: US 1999-117473P 19990127; US 1999-322732
19990528; US 2000-704321 20001102